OM nucleic - nucleic search, using sw model

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Run on: April 17, 2006, 14:44:37 ; Search time 8114 seconds
                 (without alignments)
                 1863.490 Million cell updates/sec

Title: US-10-764-553-2
Sequence: 266
Perfect score: 266
Sequence: 1 cgccgccacctcggagattc.........ggtgacgaacgtggccgagg 266

Scoring table: IDENTITY NUC
                 Gapop 10.0 , Gapext 1.0
Searched: 5883141 seqs, 2842172565 residues

Total number of hits satisfying chosen parameters: 11766282

Maximum DB seq length: 200000000
Minimum DB seq length: 0

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_in:*
                 3: gb_env:*
                 4: gb_om:*
                 5: gb_ov:*
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                 10: gb_sts:*
                 11: gb_sy:*
                 12: gb_un:*
                 13: gb_vi:*
                 14: gb_htg:*
                 15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	266	100.0	80557	6	AX704276	AX704276 Sequence
c	2	266	100.0	110000	1	AE000516_28	Continuation (29 o
c	3	266	100.0	110000	1	AE000516_29	Continuation (30 o
c	4	266	100.0	307550	1	BX248343	BX248343 Mycobacte
c	5	266	100.0	346051	1	BX842580	BX842580 Mycobacte
c	6	134.4	50.5	303855	1	AE017230	AE017230 Mycobacte
c	7	97.2	36.5	38807	1	MLCB1259	MLCB1259 Mycobacte
c	8	97.2	36.5	40429	1	U00011	U00011 Mycobacteri
c	9	97.2	36.5	40429	6	AR345357	AR345357 Sequence
c	10	97.2	36.5	344050	1	MLEPRTN2	AL583918 Mycobacte
c	11	71	26.7	110000	1	AP006618_38	Continuation (38
c	12	71	26.7	110000	1	AP006618_39	Continuation (39
c	13	69	25.9	110000	1	BA000035_18	Continuation (19 o
c	14	65.4	24.6	110000	1	BA000030_81	Continuation (82 o
c	15	64.6	24.3	4312	1	AJ505987	SGA505987 Strepto
c	16	64	24.1	348408	1	BX248358	BX248358 Corynebac
c	17	61.2	23.0	3522	1	AF421216	AF421216 Streptomy
c	18	60.6	22.8	3350	1	SCAPTRELA	X87267 S.coelicolo
c	19	60.6	22.8	110000	1	CR931997_12	Continuation (13 o
c	20	60.6	22.8	277000	1	SCO939109	AL939109 Streptomy
c	21	59.8	22.5	110000	1	AE017282_08	Continuation (9 of
c	22	59.8	22.5	110000	1	CP000090_03	Continuation (4 of
c	23	58.8	22.1	110000	1	BD164026	BD164026 Novel pol
c	24	58.8	22.1	555	6	AX121909	AX121909 Sequence
c	25	58.8	22.1	555	6	AX064737	AX064737 Sequence
c	26	58.8	22.1	678	1	AF038651	AF038651 Corynebac
c	27	58.8	22.1	13750	1	BA000036_17	Continuation (18 o
c	28	58.8	22.1	349584	1	BX927153	BX927153 Corynebac
c	29	58.8	22.1	349980	6	AX127148	AX127148 Sequence
c	30	57.4	21.6	4238	1	SCSBCAPT	SCSBCAPT Sequence
c	31	57.2	21.5	190050	1	AL646059	AL646059 Ralstonia
c	32	56.2	21.1	806	15	AK108481	AK108481 Oryza sat
c	33	56.2	21.1	110000	1	BX571965_05	Continuation (6 of
c	34	56.2	21.1	110000	1	CP000010_31	Continuation (32 o
c	35	55.4	20.8	110000	1	AP008231_17	Continuation (18 o
c	36	55	20.7	342259	1	BX640435	BX640435 Bordetell
c	37	55	20.7	342287	1	BX640450	BX640450 Bordetell
c	38	54.6	20.5	297050	1	AL935258	AL935258 Lactobaci
c	39	54.4	20.4	79370	3	UNK431260	UNK431260 Uncultur
c	40	53.6	20.2	303642	1	AE016923	AE016923 Chromoba
c	41	53.4	20.1	346359	1	BX640411	BX640411 Bordetell
c	42	52.4	19.7	110000	1	CP000009_08	Continuation (9 of
c	43	52.4	19.7	110000	1	CP000008_09	Continuation (10 o
c	44	52.2	19.6	489	6	AX432181	AX432181 Sequence
c	45	52.2	19.6	110000	1	AE017333_27	Continuation (28 o

ALIGNMENTS

RESULT 1
AX704276/c

```
LOCUS       AX704276               80557 bp    DNA     linear   PAT 03-APR-2003
DEFINITION  Sequence 647 from Patent WO02074903.
ACCESSION   AX704276
VERSION     AX704276.1  GI:29538531
KEYWORDS
SOURCE      Mycobacterium tuberculosis
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
            tuberculosis complex.
REFERENCE
  AUTHORS   Cole,S.
  TITLE     Comparative mycobacterial genomics as a tool for identifying
            targets for the diagnosis, prophylaxis or treatment of
            mycobacterioses
  JOURNAL   Patent: WO 02074903-A 647 26-SEP-2002;
            INSTITUT PASTEUR (FR)
FEATURES             Location/Qualifiers
     source          1..80557
                     /organism="Mycobacterium tuberculosis"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:1773"
                     /note="BAC-Rv234 deposited at the C.N.C.M. under the A.N.
                     I-2627"
ORIGIN

Query Match             100.0%;  Score 266;  DB 6;  Length 80557;
Best Local Similarity   100.0%;
Matches  266;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy          1 CGCCGCCACTCGGAGATTCTCGCTGAGGGCATCGAGGTTGCGGCGCCGGTGTCGTGAT  60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62589 CGCCGCCACTCGGAGATTCTCGCTGAGGGCATCGAGGTTGCGGCGCCGGTGTCGTGAT  62530

Qy         61 CATTGACGACGTGTTAGCAACCGGCGGCGCCACCATCGGCGACGCGACGCCTGCTTGAGCG  120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62529 CATTGACGACGTGTTAGCAACCGGCGGCGCCACCATCGGCGACGCGACGCCTGCTTGAGCG  62470

Qy        121 CGGTGGCGCGCCAACGTGGCCGGGGGCGCGCGCCCGTAGTGGTTGGTGGAACTTGCGGGGTTGAGGGGTCG  180
```

OM nucleic - nucleic search, using sw model

GenCore version 5.1.7
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Run on: April 17, 2006, 14:18:52 ; Search time 367 seconds
(without alignments)
4830.540 Million cell updates/sec

Title: US-10-764-553-2
Perfect score: 266
Sequence: 1 cgccgccactctggagattc.........ggtgacgaacgtggccgagg 266

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 333246308 residues
Total number of hits satisfying chosen parameters: 9993994

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database :
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2:  geneseqn1990s:*
3:  geneseqn2000s:*
4:  geneseqn2001as:*
5:  geneseqn2001bs:*
6:  geneseqn2002as:*
7:  geneseqn2002bs:*
8:  geneseqn2003as:*
9:  geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

N_Geneseq_21:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES.

	Result No.	Score	% Query Match	Match length	DB	ID	Description
	1	266	100.0	266	14	AD265097	Adz65097 Mycobacte
	2	266	100.0	1874	14	ADZ65096	Adz65096 Mycobacte
c	3	266	100.0	80557	6	ABX09142	Abx09142 Mycobacte
c	4	266	100.0	110000	4	AI199682_29	Continuation (29 o
c	5	266	100.0	110000	4	AI99683_28	Continuation (29 o
c	6	266	100.0	110000	4	AI99683_29	Continuation (30 o
c	7	.97.2	36.5	40429	10	ADB74376	Adb74376 Mycobacte
c	8	59.2	22.3	556	13	ADX09191	Adx09191 Plant ful
	9	59.2	22.3	1009	13	ADX48946	Adx48946 Plant ful
	10	59.2	22.3	1014	13	ADX52666	Adx52666 Plant ful
	11	59	22.2	595	13	ADX10366	Adx10366 Plant ful
	12	58.8	22.1	555	5	AAH66790	Aah66790 C glutami
	13	58.8	22.1	678	5	AAF72262	Aaf72262 Corynebac
c	14	58.8	22.1	349980	5	AAH68529	Aah68529 C glutami
	15	53.8	20.2	543	13	ADT43091	Adt43091 Bacterial
	16	52.2	19.6	489	6	ABK73305	Abk73305 Bacillus
	17	51.2	19.2	18477	4	AAS59634	Aas59634 Propionib
	18	51.2	19.2	18477	8	ACF64563	Acf64563 Propionib
	19	50.8	19.1	510	13	ADS56682	Ads56682 Bacterial
	20	48.6	18.3	660	11	ACH99807	Ach99807 Klebsiell
	21	48.4	18.2	450	13	ADS63368	Ads63368 Bacterial
	22	48.4	18.2	456	13	ADS63735	Ads63735 Bacterial
	23	47.2	17.7	546	13	ADS59951	Ads59951 Bacterial
	24	47	17.7	510	13	ADS55671	Ads55671 Bacterial
	25	47	17.7	516	13	ADS50157	Ads50157 Bacterial
	26	47	17.7	522	13	ADS56186	Ads56186 Bacterial
	27	46.6	17.5	516	9	ADB10513	Adb10513 Alloiococ
	28	46.6	17.5	110000	9	ADB12064_11	Continuation (12 o
	29	46.2	17.4	570	13	ADS61694	Ads61694 Bacterial
	30	46	17.3	546	13	ADS61867	Ads61867 Bacterial
c	31	45.6	17.1	552	5	ACL64706	Acl64706 M. xanthu
	32	45.2	17.0	552	10	ADE76492	Ade76492 APRT reco
	33	45.2	17.0	552	13	ADE76490	Ade76490 APRT reco
	34	45.2	17.0	552	5	ADS45994	Ads45994 Bacterial
c	35	45.2	17.0	1617	5	AAS90127	Aas90127 DNA encod
	36	45	16.9	615	13	ADT45732	Adt45732 Bacterial
	37	45	16.9	1511	13	ADT17106	Adt17106 Plant CDN
	38	44.8	16.8	1511	13	ABN67362	Abn67362 Streptoco
	39	44.8	16.8	110000	6	ABN71527_11	Continuation (12 o
	40	44.6	16.8	516	13	ADT42451	Adt42451 Bacterial
c	41	44.6	16.8	426	11	ABD07932	Abd07932 Pseudomon
c	42	44.4	16.7	504	13	ADT47054	Adt47054 Bacterial
c	43	44.4	16.7	549	10	ADJ62246	Adj62246 P_aerugin
	44	44.4	16.7	549	10	ADJ62248	Adj62248 P_aerugin
	45	44.4	16.7	549	14	AEC10906	Aec10906 Pseudomon

ALIGNMENTS

RESULT 1
AD265097
AD265097

```
ID   ADZ65097 standard; DNA; 266 BP.
XX
AC   ADZ65097;
XX
DT   14-JUL-2005 (first entry)
XX
DE   Mycobacterium tuberculosis real/spoT upstream DNA fragment.
XX
KW   promoter; high throughput screening; antibacterial; ds.
XX
OS   Mycobacterium tuberculosis.
XX
PN   US2005095252-A1.
XX
PR   27-JAN-2004; 2004US-00764553.
XX
PD   05-MAY-2005.
XX
PF   27-JAN-2003; 2003US-0442511P.
XX
PA   (COUN-) COUNCIL SCI & IND RES INDIA.
XX
PI   Chatterjee D;
XX
DR   WPI; 2005-344982/35.
XX
PT   New promoter derived from Mycobacterium tuberculosis, useful for high
PT   throughput screening and developing inhibitors of M. tuberculosis under
PT   low carbon or starved conditions.
XX
PS   Claim 1; SEQ ID NO 2; 20pp; English.
XX
CC   The invention relates to a promoter (I) for high throughput screening and
CC   developing inhibitors of Mycobacteria under low carbon or starved
CC   conditions, and having the 266 base pair sequence of ADZ65097. Also
CC   described: (1) an expression system (II) for high-throughput screening
CC   and developing inhibitors of Mycobacteria under low carbon or starved
CC   conditions, comprising of promoter of promoter of 200 base pair having
CC   vector pSAKL12; and (2) preparing a promoter expression system for high-
CC   throughput screening and developing inhibitors against Mycobacteria under
```

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OM nucleic - nucleic search, using sw model.

Run on: April 17, 2006, 14:50:53 ; Search time 2438 Seconds
          (without alignments)
          5104.743 Million cell updates/sec

Title: US-10-764-553-2
Perfect score: 266
Sequence: 1 cgccgccactcggagattc...........ggtgacgaacgtggccgagg 266

Scoring table: IDENTITY_NUC
              Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 2339541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 listing first 45 summaries

Database :   EST:*
              1: gb_est1:*
              2: gb_est2:*
              3: gb_est3:*
              4: gb_htc:*
              5: gb_est4:*
              6: gb_est5:*
              7: gb_est6:*
              8: gb_est7:*
              9: gb_gss:*
             10: gb_gss1:*
             11: gb_gss2:*
             11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
c 1	59.8	22.5	565	1	AW499392	AW499392 660053H06
c 2	59.2	22.3	411	7	AW216342	AW216342 687049G12
c 3	59.2	22.3	414	10	CW112430	CW112430 104_486_1
c 4	59.2	22.3	510	6	CB886221	CB886221 3529_1_93
c 5	59.2	22.3	530	7	CV126031	CV126031 EST5216_2
c 6	59.2	22.3	560	6	CF034861	CF034861 QCG10g05.
c 7	59.2	22.3	613	7	CK700872	CK700872 EST4973 Z
c 8	59.2	22.3	645	7	CK327504	CK327504 EST4814 Z
c 9	59.2	22.3	733	8	DN218073	DN218073 MEST1060
c 10	59	22.2	473	1	BM074175	BM074175 MEST82-D0
c 11	59	22.2	521	1	AW331541	AW331541 687041A10
c 12	59	22.2	709	6	CA400905	CA400905 ELO1N0412
c 13	59.	22.2	1021	6	AY104264	AY104264 Zea mays
c 14	57.4	21.6	728	8	DR961782	DR961782 ZM BFb007
c 15	56.6	21.3	555	1	AJ826866	AJ826866 AJ826866
c 16	56.6	21.3	576	1	AJ533349	AJ533349 AJ533349
c 17	56.6	21.3	587	1	AJ824359	AJ824359 AJ824359
c 18	56.6	21.3	604	1	AJ822179	AJ822179 AJ822179
c 19	56.6	21.3	629	5	BU040781	BU040781 PP_LEa000
c 20	56.6	21.3	684	1	AJ826935	AJ826935 AJ826935
c 21	56.6	21.3	784	1	AJ822971	AJ822971 AJ822971
c 22	56.2	21.1	771	6	CB658255	CB658255 OSJNEC14C
c 23	56.2	21.1	807	6	CB658256	CB658256 OSJNEC14C
c 24	56	21.1	489	10	CW087298	CW087298 104_431_1
c 25	56	21.1	518	1	AW066851	AW066851 6830I0B02
c 26	56	21.1	631	5	BU044866	BU044866 PP_LEa002
c 27	55	20.7	487	7	CV044141	CV044141 EST 5848
c 28	55	20.7	666	7	CV045140	CV045140 EST 6847
c 29	55	20.7	851	6	CB822288	CB822288 EST 3139
c 30	55	20.7	875	6	CB820147	CB820147 EST 1139
c 31	54.8	20.6	709	6	CA760383	CA760383 BR060004B
c 32	54	20.3	865	6	CB822819	CB822819 EST 4043
c 33	51.6	19.4	522	7	CV046024	CV046024 EST 7731
c 34	51.2	19.2	597	8	DR956887	DR956887 ZM BFb005
c 35	49.8	18.7	729	7	CV090754	CV090754 CAI789 cD
c 36	49.8	18.7	810	7	CV090513	CV090513 CAI506 cD
c 37	49.6	18.6	163	5	BQ779570	BQ779570 946122E06
c 38	49.2	18.5	486	7	CO870811	CO870811 rt63f04.y
c 39	49.2	18.5	503	7	CO871061	CO871061 rt67c02.y
c 40	49.2	18.5	617	7	CO871102	CO871102 rt67g02.Y
c 41	49.2	18.5	701	3	BI977958	BI977958 0A09 Old
c 42	49.2	18.5	717	3	BI978889	BI978889 YD04 Old
c 43	48.2	18.1	549	6	CA287880	CA287880 SCSFSD206
c 44	48.2	18.1	550	7	CN904442	CN904442 010831ABD
c 45	48.2	18.1	559	6	CF772241	CF772241 DSBP1_31

ALIGNMENTS

RESULT 1
AW499392/c
LOCUS   AW499392   565 bp   mRNA   linear   EST 01-MAR-2000
DEFINITION   660053H06.x1 660 - Mixed stages of anther and pollen Zea mays cDNA,
             mRNA sequence.
ACCESSION   AW499392
VERSION   AW499392.1   GI:7138027
KEYWORDS   EST.
SOURCE   Zea mays
  ORGANISM   Zea mays
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
             clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1 (bases 1 to 565)
  AUTHORS   Walbot,V.
  TITLE   Maize ESTs from various cDNA libraries sequenced at Stanford
             University
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Walbot V
             Department of Biological Sciences
             Stanford University
             855 California Ave, Palo Alto, CA 94304, USA
             Tel: 650 723 2227
             Fax: 650 725 8221
             Email: walbot@stanford.edu
             Plate: 660053 row: H column: 06.
FEATURES   Location/Qualifiers
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                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="Ohio43"
                     /db_xref="taxon:4577"
                     /tissue_type="whole premieotic anthers to pollen shed"
                     /dev_stage="premieotic anthers to pollen shed"
                     /lab_host="XLOLR"
                     /clone_lib="660 - Mixed stages of anther and pollen"
                     /note="Organ: anthers; Vector: Lambda Zap; Site_1: EcoRI;
                     Site_2: XhoI; Anther and pollen cDNA library.
                     Directionally sequenced with 5' end at the EcoRI site.
                     Created by Amie Franklin."
ORIGIN

Query Match   22.5%; Score 59.8; DB 1; Length 565;
Best Local Similarity   59.9%; Pred. No. 0.00029;
Matches 100; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

OM nucleic - nucleic search, using sw model

```
                            GenCore version 5.1.7
                            Copyright (c) 1993 - 2006 Biocceleration Ltd.
```

Run on: April 17, 2006, 15:45:49 ; Search time 89 Seconds

Title: US-10-764-553-2
Perfect score: 266
Sequence: 1 cgccgccactctggagattc.............ggtgacgaacgtggccgagg 266

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*

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1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/pp_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	266	100.0	4403765	3	US-09-103-840A-2	Sequence 2, Appli
2	266	100.0	4411529	3	US-09-103-840A-1	Sequence 1, Appli
3	97.2	36.5	40429	3	US-08-311-731A-125	Sequence 125, App
4	48.6	18.3	660	3	US-09-489-039A-5602	Sequence 5602, Ap
5	45.6	17.1	18538	3	US-09-902-540-1169	Sequence 1169, Ap
6	44.4	16.7	426	3	US-09-252-991A-6536	Sequence 6536, Ap
7	44.4	16.7	714	3	US-09-252-991A-6496	Sequence 6496, Ap
8	42.6	16.0	2598	3	US-09-902-540-3087	Sequence 3087, Ap
9	42.6	16.0	6898	3	US-09-902-540-862	Sequence 862, App
10	42.4	15.9	1794	3	US-09-902-540-9281	Sequence 9281, App
11	42.4	15.9	10717	3	US-09-902-540-991	Sequence 991, App
12	40.8	15.3	405	3	US-09-252-991A-7491	Sequence 7491, Ap
13	40.8	15.3	522	3	US-09-252-991A-7206	Sequence 7206, Ap
14	40.8	15.3	669	3	US-09-252-991A-7270	Sequence 7270, Ap
15	40.8	15.3	780	3	US-09-252-991A-7431	Sequence 7431, Ap
16	40.4	15.2	4403765	3	US-09-103-840A-2	Sequence 2, Appli
17	40.4	15.2	4411529	3	US-09-103-840A-1	Sequence 1, Appli
18	40.4	15.2	837	3	US-09-252-540-2787	Sequence 2787, Ap
19	40	15.0	15644	3	US-09-902-540-1133	Sequence 1133, Ap
20	39.8	15.0	855	3	US-09-252-991A-11835	Sequence 11835, A
21	39.8	15.0	1497	3	US-09-023-655-1461	Sequence 1461, Ap
22	39.8	15.0	4756	3	US-08-854-585-1	Sequence 1, Appli
23	39.8	15.0	5117	3	US-09-447-533-1	Sequence 1, Appli
24	39.8	15.0	5117	3	US-09-447-533-1	Sequence 1, Appli
25	39.8	15.0	5117	6	PCT-US95-05512-1	Sequence 1, Appli
26	39.8	15.0	7560	3	US-09-754-1112A-2	Sequence 2, Appli
27	39.8	15.0	12738	3	US-09-754-1112A-1	Sequence 1, Appli
28	39.6	14.9	903	3	US-09-902-540-9555	Sequence 9555, Ap
29	39.6	14.9	9867	3	US-09-902-540-1008	Sequence 1008, Ap
30	39.4	14.8	339	3	US-10-621-976-44	Sequence 44, Appl
31	39.4	14.8	714	3	US-10-000-489-83	Sequence 83, Appl
32	39.4	14.8	1754	3	US-10-000-489-85	Sequence 85, Appl
33	39.4	14.8	1855	3	US-11-000-489-97	Sequence 97, Appl
34	38.8	14.6	73853	3	US-09-107-532A-2574	Sequence 2574, Ap
35	38.8	14.6	534	3	US-09-949-016-12029	Sequence 12029, A
36	38.6	14.5	1710	2	US-09-912-794-1	Sequence 1, Appli
37	38.6	14.5	129658	3	US-08-758-662-4	Sequence 4, Appli
38	38.4	14.4	530	3	US-09-949-016-17195	Sequence 17195, A
39	38.4	14.4	4524	2	US-08-845-998-7	Sequence 7, Appli
40	38.4	14.4	4524	3	US-09-206-537-7	Sequence 7, Appli
41	38.4	14.4	4524	3	US-09-430-854-7	Sequence 7, Appli
42	38.2	14.4	927	3	US-09-252-991A-7558	Sequence 7558, Ap
43	38.2	14.4	1155	3	US-09-252-991A-7856	Sequence 7856, Ap
44	38	14.3	1491	3	US-09-902-540-3335	Sequence 3335, Ap
45	38	14.3	16387	3	US-09-902-540-1156	Sequence 1156, Ap

ALIGNMENTS

RESULT 1
US-09-103-840A-2/c
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
  APPLICANT: FLEISCHMAN, Robert D.
  APPLICANT: WHITE, Owen R.
  APPLICANT: FRASER, Claire M.
  APPLICANT: VENTER, John C.
  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
  TITLE OF INVENTION: TUBERCULOSIS
  FILE REFERENCE: 24366-20007.00
  CURRENT APPLICATION NUMBER: US/09/103,840A
  CURRENT FILING DATE: 1998-06-24
  NUMBER OF SEQ ID NOS: 2
  SOFTWARE: Patentin Ver. 2.1
  SEQ ID NO 2
    LENGTH: 4403765
    TYPE: DNA
    ORGANISM: Mycobacterium tuberculosis
    FEATURE:
    OTHER INFORMATION: CDC 1551
    OTHER INFORMATION:
    OTHER INFORMATION: "n" bases at various positions throughout the sequence
US-09-103-840A-2

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Best Local Similarity   100.0%; Pred. No. 8e-53;
Matches 266; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy   61 CATTGACGACGTGTTAGCAAACCGCGCGGCACCATCGAGCCGCCGCTGCTTGAGCG 120
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Qy   121 CCGGTGGCGCGCCAACGTGGCGCGGGGGCGGCGCCTAGTTGGTGGGAACTTGCCGGGGTCG 180
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Qy   241 GTCGGAGGTGACGAACGTGGCCGAGG 266
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Db 2906319 GTCGGAGGTGACGAACGTGGCCGAGG 2906320

OM nucleic - nucleic search, using sw model

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GenCore version 5.1.7

Run on: April 17, 2006, 16:09:03 ; Search time 803 Seconds
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Title: US-10-764-553-2
Perfect score: 266
Sequence: 1 cgccgccactctggagattc..........ggtgacgaacgtggccgagg 266

Scoring table: IDENTITY NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	266	100.0	1874	6	US-10-764-553-1	Sequence 1, Appli
3	266	100.0	80557	9	US-10-080-170-647	Sequence 647, Appli
4	266	100.0	80557	7	US-10-080-170-647	Sequence 647, App
5	266	100.0	80557	6	US-10-468-356-647	Sequence 647, App
6	65.4	24.6	546	6	US-10-156-761-6817	Sequence 6817, Ap
7	65.4	24.6	9025608	6	US-10-156-761-1	Sequence 1, Appli
8	59.2	22.3	448	8	US-10-425-115-63143	Sequence 63143, A
9	59.2	22.3	556	7	US-10-425-114-3766	Sequence 3766, Ap
10	59.2	22.3	1009	7	US-10-425-114-23686	Sequence 23686, A
11	59.2	22.3	1014	7	US-10-425-114-27406	Sequence 27406, A
12	59.2	22.3	1910	8	US-10-425-115-18636	Sequence 18636, A
13	59.2	22.3	595	7	US-10-425-114-4941	Sequence 4941, Ap
14	59.2	22.2	1021	8	US-10-425-115-63142	Sequence 63142, A
15	58.8	22.1	555	3	US-09-738-626-1825	Sequence 1825, Appli
16	58.8	22.1	3309400	3	US-09-738-626-1	Sequence 1, Appli
17	53.8	20.2	543	6	US-10-369-493-41529	Sequence 41529, A
18	52.2	19.6	489	3	US-09-974-300-596	Sequence 596, App
19	50.8	19.1	510	6	US-10-369-493-32356	Sequence 32356, A
20	49.8	18.7	873	7	US-10-437-963-79335	Sequence 79335, A
21	49.6	18.6	450	7	US-10-369-493-39042	Sequence 39042, A
22	48.4	18.2	456	6	US-10-369-493-39409	Sequence 39409, A
23	47.2	17.7	546	6	US-10-369-493-35625	Sequence 35625, A
24	47	17.7	510	6	US-10-369-493-31345	Sequence 31345, A
25	47	17.7	516	6	US-10-369-493-28587	Sequence 28587, A
26	47	17.7	522	6	US-10-369-493-31860	Sequence 31860, A
27	46.6	17.5	516	9	US-10-501-282-4549	Sequence 4549, Ap
28	46.6	17.5	1754382	9	US-10-501-282-6651	Sequence 6651, Ap
29	46.4	17.4	1059	8	US-10-425-115-10324	Sequence 10324, A
30	46.2	17.4	570	6	US-10-369-493-37368	Sequence 37368, A
31	46	17.3	546	6	US-10-369-493-37541	Sequence 37541, A
32	46	17.3	624	7	US-10-437-963-79373	Sequence 79373, A
33	45.6	17.1	484	8	US-10-425-115-127631	Sequence 127631,
34	45.2	17.0	552	6	US-10-369-493-24424	Sequence 24424, A
35	45.2	17.0	1617	6	US-10-369-493-25931	Sequence 25931, A
36	45	16.9	615	9	US-10-739-930-2432	Sequence 2432, Ap
37	45	16.9	1511	6	US-10-369-493-44170	Sequence 44170, A
38	44.6	16.8	504	6	US-10-369-493-40889	Sequence 40889, A
39	44.4	16.7	549	6	US-10-369-493-45492	Sequence 45492, A
40	44.4	16.7	549	6	US-10-369-493-45492	Sequence 45492, A
41	44.4	16.7	816	9	US-10-958-216-436	Sequence 436, App
42	43.8	16.5	816	9	US-10-958-216-438	Sequence 438, App
43	43.2	16.3	978	7	US-10-282-1222A-25975	Sequence 25975, A
44	43.2	16.2	520	7	US-10-767-701-555	Sequence 555, App
45	43.2	16.2	3444	6	US-10-369-493-40475	Sequence 40475, A

ALIGNMENTS

RESULT 1
US-10-764-553-2
; Sequence 2, Application US/10764553
; Publication No. US20050095252A1
; GENERAL INFORMATION:
; APPLICANT: CHATTERJEE, Deepankar
; TITLE OF INVENTION: A PROMOTER FOR HIGH-THROUGHPUT SCREENING FOR INHIBITORS AGAINST
; TITLE OF INVENTION: MYCOBACTERIA UNDER LOW CARBON CONDITIONS
; FILE REFERENCE: Q74006
; CURRENT APPLICATION NUMBER: US/10/764,553
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: US 60/442,511
; PRIOR FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 2
; LENGTH: 266
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-764-553-2

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Best Local Similarity   100.0%;
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db   1 CGCCGCCACTCTGGAGATTCTCGCTGAGGGCATCGAGGTTGCGGCGCCCGGTGTCGTGAT 60

Qy   61 CATTGACGAGCGTGTTAGCAACCGGCGGCACCATCGGCGCGCGAGGCGCCTGCTTGAGCG 120
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Db   61 CATTGACGAGCGTGTTAGCAACCGGCGGCACCATCGGCGCGCGAGGCGCCTGCTTGAGCG 120

Qy   121 CGGTGCGGCGGCCAAGTGCGGCGGCGGCGGCCGTAGTTGGTGGAACTTGCGGGGGGGTCG 180
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Db   121 CGGTGCGGCGGCCAAGTGCGGCGGCGGCGGCCGTAGTTGGTGGAACTTGCGGGGGGGTCG 180

Qy   181 CGCGGCGCTCGCACCGGCTGCCGGTGCACAGCCTGAGCCCGTGAGGGATATCCTCTAG 240
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Db   181 CGCGGCGCTCGCACCGGCTGCCGGTGCACAGCCTGAGCCCGTGAGGGATATCCTCTAG 240

Qy   241 GTCGGGAGGTGACGAAACGTGGGCCGAGG 266
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OM nucleic - nucleic search, using sw model

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Perfect score: 266
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Searched: 9281099 seqs, 2013915447 residues

Total number of hits satisfying chosen parameters: 18562198

Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	58.8	22.1	678	14	US-11-055-822-1019	Sequence 1019, Ap
2	49.4	17.4	861	11	US-11-096-568A-23747	Sequence 23747, A
3	44	16.5	970	11	US-11-096-568A-12230	Sequence 12330, A
4	41.8	15.7	1694969	7	US-10-506-454-1690	Sequence 1690, Ap
5	40	15.0	4086	11	US-11-089-508-9	Sequence 9, Appli
6	39.8	15.0	1726	14	US-11-108-528-35	Sequence 35, Appl
7	39.8	15.0	5543	8	US-10-995-561-334	Sequence 334, App
8	39.8	15.0	5548	8	US-10-995-561-335	Sequence 335, App
9	39.4	15.0	201990	8	US-10-995-561-13303	Sequence 13303, A
10	39.4	14.8	342	9	US-10-475-075-565	Sequence 565, App
11	39	14.8	912	11	US-10-995-561-10760	Sequence 10760, A
12	39	14.7	1213	11	US-11-096-568A-27146	Sequence 27146, A
13	38.6	14.5	1466	11	US-11-096-568A-24230	Sequence 24230, A
14	38.4	14.5	701	11	US-11-188-298-255	Sequence 255, App
15	38.4	14.4	1609	6	US-09-925-065A-9327	Sequence 9327, Ap
16	37.8	14.2	1609	6	US-09-925-065A-9327	Sequence 9327, Ap
17	37.8	14.2	1609	9	US-10-301-480-110564	Sequence 110564,
18	37.8	14.2	1609	10	US-10-301-480-723973	Sequence 723973,
19	37.4	14.1	524	8	US-10-775-169-17	Sequence 17, Appl
20	37.4	14.1	841	14	US-11-000-688-166	Sequence 166, App
21	37	13.9	1135	6	US-09-925-065A-698222	Sequence 698222,
22	36.8	13.8	971	7	US-10-194-487-85	Sequence 85, Appl
23	36.8	13.8	971	7	US-10-195-883-85	Sequence 85, Appl
24	36.8	13.8	971	7	US-10-195-888-85	Sequence 85, Appl
25	36.8	13.8	971	7	US-10-195-889-85	Sequence 85, Appl
26	36.8	13.8	340	6	US-09-925-065A-435303	Sequence 435303,
27	36.6	13.8	356	10	US-10-301-480-497256	Sequence 497256,
28	36.6	13.8	356	10	US-10-301-480-1110665	Sequence 1110665,
29	36.6	13.8	359	6	US-09-925-065A-435302	Sequence 435302,
30	36.6	13.8	503	6	US-09-925-065A-850757	Sequence 850757,
31	36.6	13.8	606	9	US-10-301-480-32905	Sequence 32905, A
32	36.6	13.8	606	9	US-10-301-480-32906	Sequence 32906, A
33	36.6	13.8	606	10	US-10-301-480-646314	Sequence 646314,
34	36.6	13.8	606	10	US-10-301-480-646315	Sequence 646315,
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37	36.6	13.8	1511	6	US-09-925-065A-43144	Sequence 43144, A
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ALIGNMENTS

RESULT 1
US-11-055-822-1019
Sequence 1019, Application US/11055822
Publication No. US2005026070A1
GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
FILE REFERENCE: BGI-121CPCN
CURRENT APPLICATION NUMBER: US/11/055,822
CURRENT FILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: 60/148,613
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: 60/187,970
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: 09/606,740
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/141,031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/142,101
PRIOR FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: DE 19931418.7
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931415.2
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931419.5
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931420.9
PRIOR FILING DATE: 1999-07-08
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1158
SEQ ID NO 1019
LENGTH: 678
TYPE: DNA
ORGANISM: Corynebacterium glutamicum

OM nucleic - nucleic search, using sw model

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

Run on: April 17, 2006, 15:45:49 ; Search time 89 Seconds
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Title: US-10-764-553-2
Perfect score: 266
Sequence: 1 cgccgccacctctggagattc..........ggtgacgaacgtggccgagg 266
Scoring table: IDENTITY_NUC
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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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c 2	266	100.0	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c 3	97.2	36.5	40429	3	US-08-311-731A-125	Sequence 125, App
c 4	48.6	18.3	660	3	US-09-489-039A-5602	Sequence 5602, Ap
c 5	45.6	17.1	18538	3	US-09-902-540-1169	Sequence 1169, Ap
c 6	44.4	16.7	426	3	US-09-252-991A-6536	Sequence 6536, Ap
c 7	44.4	16.7	714	3	US-09-252-991A-6496	Sequence 6496, Ap
c 8	42.6	16.0	2598	3	US-09-902-540-3087	Sequence 3087, Ap
c 9	42.6	16.0	6898	3	US-09-902-540-862	Sequence 862, App
c 10	42.6	16.0	1794	3	US-09-902-540-9281	Sequence 9281, Ap
c 11	42.4	15.9	10717	3	US-09-902-540-991	Sequence 991, App
c 12	40.8	15.3	405	3	US-09-252-991A-7491	Sequence 7491, Ap
c 13	40.8	15.3	522	3	US-09-252-991A-7206	Sequence 7206, Ap
c 14	40.8	15.3	669	3	US-09-252-991A-7270	Sequence 7270, Ap
c 15	40.8	15.3	780	3	US-09-252-991A-7431	Sequence 7431, Ap
c 16	40.4	15.2	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c 17	40.4	15.2	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c 18	40	15.0	837	3	US-09-902-540-2787	Sequence 2787, Ap
c 19	40	15.0	15644	3	US-09-902-540-1133	Sequence 1133, Ap
c 20	39.8	15.0	855	3	US-09-252-991A-11835	Sequence 11835, A
c 21	39.8	15.0	1497	3	US-09-252-991A-11611	Sequence 11611, A
c 22	39.8	15.0	4756	3	US-09-023-655-1461	Sequence 1461, Ap
c 23	39.8	15.0	5117	3	US-08-854-585-1	Sequence 1, Appli
c 24	39.8	15.0	5117	3	US-09-447-533-1	Sequence 1, Appli
c 25	39.8	15.0	5117	6	PCT-US95-05512-1	Sequence 1, Appli
c 26	39.8	15.0	7560	3	US-09-754-112A-2	Sequence 2, Appli
c 27	39.8	15.0	12738	3	US-09-754-112A-1	Sequence 1, Appli
c 28	39.6	14.9	903	3	US-09-902-540-9555	Sequence 9555, Ap
c 29	39.6	14.9	9867	3	US-09-902-540-1008	Sequence 1008, Ap
c 30	39.4	14.8	339	3	US-09-621-976-44	Sequence 44, Appl
c 31	39.4	14.8	1754	3	US-10-000-489-83	Sequence 83, Appl
c 32	39.4	14.8	1754	3	US-10-000-489-85	Sequence 85, Appl
c 33	39.4	14.8	1855	3	US-10-000-489-97	Sequence 97, Appl
c 34	38.8	14.6	1155	3	US-09-949-016-12029	Sequence 12029, A
c 35	38.8	14.5	534	3	US-09-107-532A-2574	Sequence 2574, Ap
c 36	38.6	14.5	1710	2	US-08-912-794-1	Sequence 1, Appli
c 37	38.6	14.5	129658	3	US-09-949-016-17195	Sequence 17195, A
c 38	38.4	14.4	530	3	US-08-758-662-4	Sequence 4, Appli
c 39	38.4	14.4	4524	2	US-08-845-998-7	Sequence 7, Appli
c 39	38.4	14.4	4524	3	US-09-206-537-7	Sequence 7, Appli
c 40	38.4	14.4	4524	3	US-09-430-854-7	Sequence 7, Appli
c 41	39.4	14.4	927	3	US-09-252-991A-7558	Sequence 7558, Ap
c 42	38.2	14.4	4524	3	US-09-252-991A-7856	Sequence 7856, Ap
c 43	38.2	14.4	1155	3	US-09-902-540-3335	Sequence 3335, Ap
c 44	38	14.3	1491	3	US-09-902-540-1156	Sequence 1156, Ap
c 45	38	14.3	16387	3	US-09-902-540-1156	Sequence 1156, Ap

ALIGNMENTS

RESULT 1
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMANN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match   100.0%; Score 266; DB 3; Length 4403765;
Best Local Similarity   100.0%; Pred. No. 8e-53;
Matches 266; Conservative   0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CGCCGCCACTCTGGAGATTCTCGCTCGCTGAGGGGCATCGAGGTTGGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2906559 CGCCGCCACTCTGGAGATTCTCGCTCGCTGAGGGGCATCGAGGTTGGGG 2906500

Qy   61 CATTGACGACGTGTTAGCAACCGGCGCACCATCGGCGCGGACCGCGCTTGAGCG 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2906499 CATTGACGACGTGTTAGCAACCGGCGCACCATCGGCGCGGACCGCGCTTGAGCG 2906440

Qy   121 CGGTGGCGCCAACGTGGCCCGGGGCGCCGGTAGTGGTGGAACTTGCGGGGTTGA 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2906439 CGGTGGCGCCAACGTGGCCCGGGGCGCCGGTAGTGGTGGAACTTGCGGGGTTGA 2906380

Qy   181 CGGCGGGCCTCGCACCCGCTGCCGGTGCACAGCGCCGCCTTGTGACGGGATATCCTCTAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2906379 CGGCGGGCCTCGCACCCGCTGCCGGTGCACAGCGCCGCCTTGTGACGGGATATCCTCTAG 2906320

Qy   241 GTCGGAGGTGACGAACGTGGCCGAGG 266
              ||||||||||||||||||||||||||
Db   2906319 GTCGGAGGTGACGAACGTGGCCGAGG 266

Db   2906319 GTCGGAGGTGACGAACGTGGCCGAGG 2906294

RESULT 2
US-09-103-840A-1/c
Sequence 1, Application US/09103840A
Patent No. 629432B

GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match   100.0%; Score 266; DB 3; Length 4411529;
Best Local Similarity   100.0%; Pred. No. 8e-53;
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CGGCCGCCACTCTGGAGATTCTCGCTGCTGAGGGTTGCGGGCGCCGCCGTGTCGTGAT 60
Db 2910452 CGGCCGCCACTCTGGAGATTCTCGCTGCTGAGGGTTGCGGGCGCCGCCGTGTCGTGAT 2910393
Qy   61 CATTGACGAGGTGTTAGCAACCGGCGCACCATCGCGGCGCGGACGCGCTCGGCTTGAGCG 120
Db 2910392 CATTGACGAGGTGTTAGCAACCGGCGCACCATCGCGGCGCGGACGCGCTCGGCTTGAGCG 2910333
Qy   121 CGGTGGCGCGCCAACGTGGCCGGGGCGGCCGTAGTGGTGGAACTTGCGGGGGGGTCG 180
Db 2910332 CGGTGGCGCGCCAACGTGGCCGGGGCGGCCGTAGTGGTGGAACTTGCGGGGGGGTCG 2910273
Qy   181 CGGCGCGCGCTCGCACCGCTGCGGGTGCGACAGCCTGTGTAGGGAGATATCCTCTAG 240
Db 2910272 CGGCGCGCGCTCGCACCGCTGCGGGTGCGACAGCCTGTGTAGGGAGATATCCTCTAG 2910213
Qy   241 GTCCGAGGTGACGAACGTGCCCGAGG 266
Db 2910212 GTCCGAGGTGACGAACGTGCCCGAGG 2910187

RESULT 3
US-08-311-731A-125/c
Sequence 125, Application US/08311731A
Patent No. 6583266

GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LEPRAE FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GRENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40429 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: MYCOBACTERIUM LEPRAE
US-08-311-731A-125

Query Match   36.5%; Score 97.2; DB 3; Length 40429;
Best Local Similarity   68.3%; Pred. No. 1e-13;
Matches 149; Conservative 0; Mismatches 68; Indels 1; Gaps 1;

Qy   4 CCCCACTCTGGAGATTCTCGCTGCTGAGGGCCATGGAGGTTGCGGGCGCCGCCGTGTCGTGATCAT 63
Db   9392 CGGCCATCATCGAGGTACCCGCTGACGAGCTACCGGTCGGCGCGGACAGCCGCAACGTGGCTGATTAT 9333
Qy   64 TGACGAGGTGTTAGCAACCGGCGCACCATCGCGGCGCGGACGCGCTCGGCTTGAGCCGG 123
Db   9332 TGACGACGTCTTGGCGACTGCCGGACCACTCTCGGGTGTTGGTGGTGTCCGATTATTGGGAGCGCAG 9273
Qy   124 TGGCGCGCCAACGTGGCCGGGGGCGGGCCGTA-GTGGTGGAACTTGCGGGGGGGTCGCCG 182
Db   9272 CGGGTCCGGTGGCCATTGCCGGCGGGCGGTTAGGTTTATGGAACTCACGGCGTCGGGGTCGCG 9213
Qy   183 CGGGCGCTCGCACCGCTGCGGGTGCGACAGCCTGTGCACAGCCTGAGCGCGC 220
Db   9212 AGGGCGATCGCACGGCTGCAGGTACAAAAGTTTGAGCCCC 9175

RESULT 4
US-09-489-039A-5602
Sequence 5602, Application US/0489039A
Patent No. 6610836

GENERAL INFORMATION:
; APPLICANT: Gary Breton et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 5602
; LENGTH: 660
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-5602

Query Match   18.3%; Score 48.6; DB 3; Length 660;
Best Local Similarity   54.3%; Pred. No. 0.015;
Matches 121; Conservative 0; Mismatches 99; Indels 3; Gaps 1;

Qy   1 CGGCCGCCACTCTGGAGATTCTCGCTGCTGAGGGTTGCGGGCGCCGCCGTGTCGTGAT 60